

SEQUENCE LISTING

The nucleotide sequence (SEQ ID NO:1) and deduced amino acid sequence (SEQ ID NO:2) of *Pseudomonas* exotoxin A are:

008240 "28929460

5	GCC	GAA	GAA	GCT	TTC	GAC	CTC	TGG	AAC	GAA	TGC	GCC	AAA	GCC	TGC	GTG	48
	Ala	Glu	Glu	Ala	Phe	Asp	Leu	Trp	Asn	Glu	Cys	Ala	Lys	Ala	Cys	Val	
	1				5					10					15		
10	CTC	GAC	CTC	AAG	GAC	GGC	GTG	CGT	TCC	AGC	CGC	ATG	AGC	GTC	GAC	CCG	96
	Leu	Asp	Leu	Lys	Asp	Gly	Val	Arg	Ser	Ser	Arg	Met	Ser	Val	Asp	Pro	
				20					25					30			
15	GCC	ATC	GCC	GAC	ACC	AAC	GGC	CAG	GGC	GTG	CTG	CAC	TAC	TCC	ATG	GTC	144
	Ala	Ile	Ala	Asp	Thr	Asn	Gly	Gln	Gly	Val	Leu	His	Tyr	Ser	Met	Val	
			35				40						45				
20	CTG	GAG	GGC	GGC	AAC	GAC	GCG	CTC	AAG	CTG	GCC	ATC	GAC	AAC	GCC	CTC	192
	Leu	Glu	Gly	Gly	Asn	Asp	Ala	Leu	Lys	Leu	Ala	Ile	Asp	Asn	Ala	Leu	
		50					55					60					
25	AGC	ATC	ACC	AGC	GAC	GGC	CTG	ACC	ATC	CGC	CTC	GAA	GGC	GGC	GTC	GAG	240
	Ser	Ile	Thr	Ser	Asp	Gly	Leu	Thr	Ile	Arg	Leu	Glu	Gly	Gly	Val	Glu	
	65					70					75					80	
30	CCG	AAC	AAG	CCG	GTG	CGC	TAC	AGC	TAC	ACG	CGC	CAG	GCG	CGC	GGC	AGT	288
	Pro	Asn	Lys	Pro	Val	Arg	Tyr	Ser	Tyr	Thr	Arg	Gln	Ala	Arg	Gly	Ser	
					85					90					95		
35	TGG	TCG	CTG	AAC	TGG	CTG	GTA	CCG	ATC	GGC	CAC	GAG	AAG	CCC	TCG	AAC	336
	Trp	Ser	Leu	Asn	Trp	Leu	Val	Pro	Ile	Gly	His	Glu	Lys	Pro	Ser	Asn	
				100					105					110			
40	ATC	AAG	GTG	TTC	ATC	CAC	GAA	CTG	AAC	GCC	GGC	AAC	CAG	CTC	AGC	CAC	384
	Ile	Lys	Val	Phe	Ile	His	Glu	Leu	Asn	Ala	Gly	Asn	Gln	Leu	Ser	His	
			115					120					125				
45	ATG	TCG	CCG	ATC	TAC	ACC	ATC	GAG	ATG	GGC	GAC	GAG	TTG	CTG	GCG	AAG	432
	Met	Ser	Pro	Ile	Tyr	Thr	Ile	Glu	Met	Gly	Asp	Glu	Leu	Leu	Ala	Lys	
		130					135					140					
50	CTG	GCG	CGC	GAT	GCC	ACC	TTC	TTC	GTC	AGG	GCG	CAC	GAG	AGC	AAC	GAG	480
	Leu	Ala	Arg	Asp	Ala	Thr	Phe	Phe	Val	Arg	Ala	His	Glu	Ser	Asn	Glu	
		145				150					155					160	
55	ATG	CAG	CCG	ACG	CTC	GCC	ATC	AGC	CAT	GCC	GGG	GTC	AGC	GTG	GTC	ATG	528
	Met	Gln	Pro	Thr	Leu	Ala	Ile	Ser	His	Ala	Gly	Val	Ser	Val	Val	Met	
					165					170					175		
60	GCC	CAG	ACC	CAG	CCG	CGC	CGG	GAA	AAG	CGC	TGG	AGC	GAA	TGG	GCC	AGC	576
	Ala	Gln	Thr	Gln	Pro	Arg	Arg	Glu	Lys	Arg	Trp	Ser	Glu	Trp	Ala	Ser	
				180					185					190			
65	GGC	AAG	GTG	TTG	TGC	CTG	CTC	GAC	CCG	CTG	GAC	GGG	GTC	TAC	AAC	TAC	624
	Gly	Lys	Val	Leu	Cys	Leu	Leu	Asp	Pro	Leu	Asp	Gly	Val	Tyr	Asn	Tyr	
			195					200					205				
70	CTC	GCC	CAG	CAA	CGC	TGC	AAC	CTC	GAC	GAT	ACC	TGG	GAA	GGC	AAG	ATC	672
	Leu	Ala	Gln	Gln	Arg	Cys	Asn	Leu	Asp	Asp	Thr	Trp	Glu	Gly	Lys	Ile	
		210				215						220					
75	TAC	CGG	GTG	CTC	GCC	GGC	AAC	CCG	GCG	AAG	CAT	GAC	CTG	GAC	ATC	AAA	720
	Tyr	Arg	Val	Leu	Ala	Gly	Asn	Pro	Ala	Lys	His	Asp	Leu	Asp	Ile	Lys	
		225				230					235					240	

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5	CCC Pro	ACG Thr	GTC Val	ATC Ile	AGT Ser 245	CAT His	CGC Arg	CTG Leu	CAC His	TTT Phe 250	CCC Pro	GAG Glu	GGC Gly	GGC Gly	AGC Ser 255	CTG Leu	768
	GCC Ala	GCG Ala	CTG Leu	ACC Thr 260	GCG Ala	CAC His	CAG Gln	GCT Ala	TGC Cys 265	CAC His	CTG Leu	CCG Pro	CTG Leu	GAG Glu 270	ACT Thr	TTC Phe	816
10	ACC Thr	CGT Arg	CAT His 275	CGC Arg	CAG Gln	CCG Pro	CGC Arg	GGC Gly 280	TGG Trp	GAA Glu	CAA Gln	CTG Leu	GAG Glu 285	CAG Gln	TGC Cys	GGC Gly	864
15	TAT Tyr	CCG Pro	GTG Val 290	CAG Gln	CGG Arg	CTG Leu	GTC Val 295	GCC Ala	CTC Leu	TAC Tyr	CTG Leu	GCG Ala 300	GCG Ala	CGG Arg	CTG Leu	TCG Ser	912
20	TGG Trp 305	AAC Asn	CAG Gln	GTC Val	GAC Asp	CAG Gln 310	GTG Val	ATC Ile	CGC Arg	AAC Asn 315	GCC Ala	CTG Leu	GCC Ala	AGC Ser	CCC Pro	GGC Gly 320	960
25	AGC Ser	GGC Gly	GGC Gly	GAC Asp	CTG Leu 325	GGC Gly	GAA Glu	GCG Ala	ATC Ile	CGC Arg 330	GAG Glu	CAG Gln	CCG Pro	GAG Glu	CAG Gln 335	GCC Ala	1008
	CGT Arg	CTG Leu	GCC Ala	CTG Leu 340	ACC Thr	CTG Leu	GCC Ala	GCC Ala	GCC Ala 345	GAG Glu	AGC Ser	GAG Glu	CGC Arg	TTC Phe 350	GTC Val	CGG Arg	1056
30	CAG Gln	GGC Gly	ACC Thr 355	GGC Gly	AAC Asn	GAC Asp	GAG Glu	GCC Ala 360	GGC Gly	GCG Ala	GCC Ala	AAC Asn	GCC Ala 365	GAC Asp	GTG Val	GTG Val	1104
35	AGC Ser	CTG Leu 370	ACC Thr	TGC Cys	CCG Pro	GTC Val	GCC Ala 375	GCC Ala	GGT Gly	GAA Glu	TGC Cys	GCG Ala 380	GGC Gly	CCG Pro	GCG Ala	GAC Asp	1152
40	AGC Ser 385	GGC Gly	GAC Asp	GCC Ala	CTG Leu	CTG Leu 390	GAG Glu	CGC Arg	AAC Asn	TAT Tyr	CCC Pro 395	ACT Thr	GGC Gly	GCG Ala	GAG Glu	TTC Phe 400	1200
	CTC Leu	GGC Gly	GAC Asp	GGC Gly 405	GAC Asp	GTC Val	AGC Ser	TTC Phe	AGC Ser 410	ACC Thr	CGC Arg	GGC Gly	ACG Thr	CAG Gln 415	AAC Asn		1248
45	TGG Trp	ACG Thr	GTG Val	GAG Glu 420	CGG Arg	CTG Leu	CTC Leu	CAG Gln	GCG Ala 425	CAC His	CGC Arg	CAA Gln	CTG Leu	GAG Glu 430	GAG Glu	CGC Arg	1296
50	GGC Gly	TAT Tyr	GTG Val 435	TTC Phe	GTC Val	GGC Gly	TAC Tyr	CAC His 440	GGC Gly	ACC Thr	TTC Phe	CTC Leu	GAA Glu 445	GCG Ala	GCG Ala	CAA Gln	1344
55	AGC Ser	ATC Ile 450	GTC Val	TTC Phe	GGC Gly	GGG Gly 455	GTG Val	CGC Arg	GCG Ala	CGC Arg	AGC Ser	CAG Gln 460	GAC Asp	CTC Leu	GAC Asp	GCG Ala	1392
60	ATC Ile 465	TGG Trp	CGC Arg	GGT Gly	TTC Phe	TAT Tyr 470	ATC Ile	GCC Ala	GGC Gly	GAT Asp	CCG Pro 475	GCG Ala	CTG Leu	GCC Ala	TAC Tyr	GGC Gly 480	1440
	TAC Tyr	GCC Ala	CAG Gln	GAC Asp	CAG Gln 485	GAA Glu	CCC Pro	GAC Asp	GCA Ala	CGC Arg 490	GGC Gly	CGG Arg	ATC Ile	CGC Arg	AAC Asn 495	GGT Gly	1488
65	GCC Ala	CTG Leu	CTG Leu	CGG Arg 500	GTC Val	TAT Tyr	GTG Val	CCG Pro	CGC Arg 505	TCG Ser	AGC Ser	CTG Leu	CCG Pro	GGC Gly 510	TTC Phe	TAC Tyr	1536

	CGC	ACC	AGC	CTG	ACC	CTG	GCC	GCG	CCG	GAG	GCG	GCG	GGC	GAG	GTC	GAA	1584
	Arg	Thr	Ser	Leu	Thr	Leu	Ala	Ala	Pro	Glu	Ala	Ala	Gly	Glu	Val	Glu	
			515					520					525				
5	CGG	CTG	ATC	GGC	CAT	CCG	CTG	CCG	CTG	GCG	CTG	GAC	GCC	ATC	ACC	GGC	1632
	Arg	Leu	Ile	Gly	His	Pro	Leu	Pro	Leu	Arg	Leu	Asp	Ala	Ile	Thr	Gly	
		530					535					540					
10	CCC	GAG	GAG	GAA	GGC	GGG	CGC	CTG	GAG	ACC	ATT	CTC	GGC	TGG	CCG	CTG	1680
	Pro	Glu	Glu	Glu	Gly	Gly	Arg	Leu	Glu	Thr	Ile	Leu	Gly	Trp	Pro	Leu	
		545				550					555					560	
15	GCC	GAG	CGC	ACC	GTG	GTG	ATT	CCC	TCG	GCG	ATC	CCC	ACC	GAC	CCG	CGC	1728
	Ala	Glu	Arg	Thr	Val	Val	Ile	Pro	Ser	Ala	Ile	Pro	Thr	Asp	Pro	Arg	
					565					570					575		
20	AAC	GTC	GGC	GGC	GAC	CTC	GAC	CCG	TCC	AGC	ATC	CCC	GAC	AAG	GAA	CAG	1776
	Asn	Val	Gly	Gly	Asp	Leu	Asp	Pro	Ser	Ser	Ile	Pro	Asp	Lys	Glu	Gln	
				580					585					590			
25	GCG	ATC	AGC	GCC	CTG	CCG	GAC	TAC	GCC	AGC	CAG	CCC	GGC	AAA	CCG	CCG	1824
	Ala	Ile	Ser	Ala	Leu	Pro	Asp	Tyr	Ala	Ser	Gln	Pro	Gly	Lys	Pro	Pro	
			595					600					605				
30	CGC	GAG	GAC	CTG	AAG												1839
	Arg	Glu	Asp	Leu	Lys												
		610															

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